APPENDIX A

ALIGN calculates a global alignment of two sequences version 2.0uPlease cite: Myers and Miller, CABIOS (1989) >US20040081980 SEQ ID NO:10 642 aa vs. >US 10/674,636 SEQ ID NO:2 581 aa scoring matrix: BLOSUM50, gap penalties: -12/-2 66.9% identity; Global alignment score: 3612							
/ //tmp/s	10 MVVVPFTIPFDSSVW	LLQKLNSPWI	30 RMTVDYHTLN	40 QAVTLIIAAVL	50 GVASLLEQO	60 GFSRAIW	
SEQ	MPQGLTSSASQWCF			:::: . : FLILQPLLGHRQW 20			
/tmp/s	70 ENRESLSKVCVSQGP		90 GDIKVQGGPS		110 WIQGKQVT\	120 ⁄LGSPVP	
SEQ	: . GKT 30		::::::::::::::::::::::::::::::::::::::				
SEQ	130 VNVFLGVPFAAPPLG :::::::::: VNVFLGVPFAAPPLG 50 70	SLRFTNPQPA	:::::::: ASPWDNLREA	TSYPNLCLQNS :::::::: TSYPNLCLQNS	EWLLLDQHI EWLLLDQHI	::::::	
SEQ	190 KFGVSEDCLYLNIYA :::::::::: KFGVSEDCLYLNIYA 20 130	PAHADTGSKI	LPVLVWFPGG	::::::::::::	GSALAAYEI	::::::	
SEQ	250 QYRLGIFGFFTTWDQ ::::::::: QYRLGIFGFFTTWDQ 30 190	HAPGNWAFKI ::::::::: HAPGNWAFKI	OQVAALSWVQ	:::::::: KNIEFFGGDPS	SVTIFGES	::::::	
SEQ	310 SLILSPMAKGLFHKA ::::::::: SLILSPMAKGLFHKA 40 250	::::::::	PYLEAHDYEK	SEDLQVVAHFO	:::::::	::::::	
SEQ	370 TKPSKELLTLSQKTK ::::::::: TKPSKELLTLSQKTK 00 310	::::::::	::::::::	::::::::::	:::::::	::::::	
SEQ	430 EAPEVLSGSNKSLAL :::::::::: EAPEILSGSNKSLAL 60 370	::::::::	::::::::	::::::::::	:::::::	::::::	

Attorney Docket Number: MPI00-524P1RDV1M

/tmp/s VPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVM SEQ VPALITARYHRDAGAPVYFYEFRHRPQCFEDTKPAFVKADHADEVRFVFGGAFLKGDIVM /tmp/s FEGATEEEKLLSRKMMKYWATFARTGNPNGNDLFLWPAYNLTEQYLQLDLNMSLGQRLKE SEQ FEGATEEEKLLSRKMMKYWATFARTGNPNGNDLSLWPAYNLTEQYLQLDLNMSLGQRLKE /tmp/s PRVEFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP SEO PRVDFWTSTIPLILSASDMLHSPLSSLTFLSLLQPFFFFCAP

Serial Number: <u>10/674,636</u>